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AUG 20 2002

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9

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/673,166

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If **Intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
→ Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,166

DATE: 08/19/2002

TIME: 12:54:26

Input Set : A:\102.174.txt

Output Set: N:\CRF3\08192002\I673166.raw

3 <110> APPLICANT: Le Gal, Frederique Anne
 4 Guillet, Jean Gerard
 5 Gahery-Segard, Hanne
 6 Gras-Masse, Helene
 7 Melnik, Oleg
 8 Tartar, Andre

10 <120> TITLE OF INVENTION: LIPOPEPTIDES INDUCING T LYMPHOCYTIC CYTOTOXICITY
 11 BEARING AT LEAST ONE AUXILIARY T EPITOPE, AND USES FOR
 12 VACCINATION

13 <130> FILE REFERENCE: 102.174
 14 <140> CURRENT APPLICATION NUMBER: 09/673,166
 15 <141> CURRENT FILING DATE: 2001-04-04
 16 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00792
 17 <151> PRIOR FILING DATE: 1999-04-06
 18 <160> NUMBER OF SEQ ID NOS: 276
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 14
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Clostridium tetanus
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: amino acids 830-843 of the tetanus toxin
 26 <400> SEQUENCE: 1
 27 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 28 1 5 10
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 14
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Human Papillomavirus (HPV)
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: amino acids 43-57 of HPV E7 protein
 35 <400> SEQUENCE: 2
 36 Gly Gln Ala Glu Pro Asp Arg Ala His Asn Ile Val Thr Phe
 37 1 5 10
 38 <210> SEQ ID NO: 3
 39 <211> LENGTH: 28
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <221> NAME/KEY: LIPID
 44 <222> LOCATION: (1)
 45 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue
 46 <400> SEQUENCE: 3

Does Not Comply
 Corrected Diskette Needed

JN 1-3

(see item 11 on Exam
 Summary Sheet)

The source of genetic material
 for the entire
 Artificial
 Sequence needs
 to be
 explained. 8 19 02

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63 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 64 1 5 10 15
 65 Ala Ala Ala Ala Gly Ile Gly Ile Leu Thr Val
 66 20 25
 70 <210> SEQ ID NO: 4
 71 <211> LENGTH: 28
 72 <212> TYPE: PRT
 73 <213> ORGANISM: Artificial Sequence
 75 <220> FEATURE:
 76 <221> NAME/KEY: LIPID
 77 <222> LOCATION: (1)
 78 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue
 80 <400> SEQUENCE: 4
 81 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 82 1 5 10 15
 83 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
 84 20 25
 88 <210> SEQ ID NO: 5
 89 <211> LENGTH: 28
 90 <212> TYPE: PRT
 91 <213> ORGANISM: Artificial Sequence
 93 <220> FEATURE:
 94 <221> NAME/KEY: LIPID
 95 <222> LOCATION: (1)
 96 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue
 98 <400> SEQUENCE: 5
 99 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 100 1 5 10 15
 102 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
 103 20 25
 106 <210> SEQ ID NO: 6
 107 <211> LENGTH: 28
 108 <212> TYPE: PRT
 109 <213> ORGANISM: Artificial Sequence
 111 <220> FEATURE:
 112 <221> NAME/KEY: LIPID
 113 <222> LOCATION: (1)
 114 <223> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue
 116 <400> SEQUENCE: 6
 117 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 118 1 5 10 15
 120 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
 121 20 25
 124 <210> SEQ ID NO: 7
 125 <211> LENGTH: 28
 126 <212> TYPE: PRT
 127 <213> ORGANISM: Artificial Sequence
 129 <220> FEATURE:
 130 <221> NAME/KEY: LIPID

entire sequence needs to be explained

same error

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131 <222> LOCATION: (1)
 132 <223> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue
 134 <400> SEQUENCE: 7

135 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 136 1 5 10 15

138 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
 139 20 25

142 <210> SEQ ID NO: 8

143 <211> LENGTH: 10

144 <212> TYPE: PRT

145 <213> ORGANISM: Artificial Sequence

147 <220> FEATURE:

148 <223> OTHER INFORMATION: A hydrazine is bound between the N-terminal lysine
 149 and isoleucine at position 2

151 <400> SEQUENCE: 8

152 Lys Ile Leu Lys Glu Pro Val His Gly Val
 153 1 5 10

156 <210> SEQ ID NO: 9

157 <211> LENGTH: 15

158 <212> TYPE: PRT

159 <213> ORGANISM: Artificial Sequence

161 <220> FEATURE:

162 <223> OTHER INFORMATION: aldehyde group bound to N-terminal residue

164 <220> FEATURE:

165 <221> NAME/KEY: LIPID

166 <222> LOCATION: (15)

167 <223> OTHER INFORMATION: palmitoyl chain on C-terminal lysine residue

169 <400> SEQUENCE: 9

170 Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Lys
 171 1 5 10 15

174 <210> SEQ ID NO: 10

175 <211> LENGTH: 9

176 <212> TYPE: PRT

177 <213> ORGANISM: Homo sapiens

179 <220> FEATURE:

180 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 181 myeloid leukemia translocation)

183 <400> SEQUENCE: 10

184 Glu Asp Ala Glu Leu Asn Pro Arg Phe
 185 1 5

188 <210> SEQ ID NO: 11

189 <211> LENGTH: 9

190 <212> TYPE: PRT

191 <213> ORGANISM: Homo sapiens

193 <220> FEATURE

194 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 195 myeloid leukemia translocation)

197 <400> SEQUENCE: 11

198 Ser Glu Leu Asp Leu Glu Lys Gly Leu

Please correct this error
 in subsequent sequences

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199 1 5
 202 <210> SEQ ID NO: 12
 203 <211> LENGTH: 9
 204 <212> TYPE: PRT
 205 <213> ORGANISM: Homo sapiens
 207 <220> FEATURE:
 208 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 209 myeloid leukemia translocation)
 211 <400> SEQUENCE: 12
 212 Asp Glu Leu Glu Ala Val Pro Asn Ile
 213 1 5
 216 <210> SEQ ID NO: 13
 217 <211> LENGTH: 9
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Homo sapiens
 221 <220> FEATURE:
 222 <223> OTHER INFORMATION: epitope from BCF-ABL fusion protein (chronic
 223 myeloid leukemia translocation)
 225 <400> SEQUENCE: 13
 226 Lys Glu Asp Ala Leu Gln Arg Pro Val
 227 1 5
 230 <210> SEQ ID NO: 14
 231 <211> LENGTH: 9
 232 <212> TYPE: PRT
 233 <213> ORGANISM: Homo sapiens
 235 <220> FEATURE:
 236 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 237 myeloid leukemia translocation)
 239 <400> SEQUENCE: 14
 240 Glu Asp Ala Leu Gln Arg Pro Val Ala
 241 1 5
 244 <210> SEQ ID NO: 15
 245 <211> LENGTH: 9
 246 <212> TYPE: PRT
 247 <213> ORGANISM: Homo sapiens
 249 <220> FEATURE:
 250 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 251 myeloid leukemia translocation)
 253 <400> SEQUENCE: 15
 254 Gly Glu Lys Leu Arg Val Leu Gly Tyr
 255 1 5
 258 <210> SEQ ID NO: 16
 259 <211> LENGTH: 9
 260 <212> TYPE: PRT
 261 <213> ORGANISM: Homo sapiens
 263 <220> FEATURE:
 264 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 265 myeloid leukemia translocation)
 267 <400> SEQUENCE: 16

RAW SEQUENCE LISTING

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268 Glu Asp Thr Met Glu Val Glu Glu Phe
 269 1 5
 270 <210> SEQ ID NO: 17
 271 <211> LENGTH: 9
 272 <212> TYPE: PRT
 273 <213> ORGANISM: Homo sapiens
 274 <220> FEATURE:
 275 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 276 myeloid leukemia translocation)
 281 <400> SEQUENCE: 17
 282 Met Glu Tyr Leu Glu Lys Lys Asn Phe
 283 1 5
 286 <210> SEQ ID NO: 18
 287 <211> LENGTH: 9
 288 <212> TYPE: PRT
 289 <213> ORGANISM: Homo sapiens
 291 <220> FEATURE:
 292 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 293 myeloid leukemia translocation)
 295 <400> SEQUENCE: 18
 296 Asn Glu Glu Ala Ala Asp Glu Val Phe
 297 1 5
 300 <210> SEQ ID NO: 19
 301 <211> LENGTH: 9
 302 <212> TYPE: PRT
 303 <213> ORGANISM: Homo sapiens
 305 <220> FEATURE:
 306 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 307 myeloid leukemia translocation)
 309 <400> SEQUENCE: 19
 310 Val Asn Gln Glu Arg Phe Arg Met Ile
 311 1 5
 314 <210> SEQ ID NO: 20
 315 <211> LENGTH: 9
 316 <212> TYPE: PRT
 317 <213> ORGANISM: Homo sapiens
 319 <220> FEATURE:
 320 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 321 myeloid leukemia translocation)
 323 <400> SEQUENCE: 20
 324 Leu Phe Gln Lys Leu Ala Ser Gln Leu
 325 1 5
 328 <210> SEQ ID NO: 21
 329 <211> LENGTH: 9
 330 <212> TYPE: PRT
 331 <213> ORGANISM: Homo sapiens
 333 <220> FEATURE:
 334 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
 335 myeloid leukemia translocation)

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